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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/043,649

DATE: 12/02/2002

TIME: 15:08:54

Input Set : A:\EP.txt

Output Set: N:\CRF4\12022002\J043649.raw

3 <110> APPLICANT: Holland, Sacha J.
 4 Mendenhall, Marcy K.
 5 Pardo, Jorge
 6 Spencer, Collin
 7 Fu, C. Alan
 8 Luo, Ying
 9 Payan, Donald G.
 10 Mancebo, Helena S.Y.
 11 Wu, Jun
 12 Zhou, Xiulan
 13 Shen, Mary
 14 Liao, X. Charlene
 15 Sheng, Ning
 17 <120> TITLE OF INVENTION: Cloning of a Novel Inhibitor of Antigen-receptor Signalling

by a

18 Retroviral-based Functional Screen
 20 <130> FILE REFERENCE: A-70219-1/RMS/DHR
 22 <140> CURRENT APPLICATION NUMBER: US 10/043,649
 23 <141> CURRENT FILING DATE: 2002-01-10
 25 <150> PRIOR APPLICATION NUMBER: US 60/260,953
 26 <151> PRIOR FILING DATE: 2001-01-10
 28 <160> NUMBER OF SEQ ID NOS: 3
 30 <170> SOFTWARE: PatentIn version 3.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 786
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (1)..(786)
 40 <223> OTHER INFORMATION:

W--> 42 <400> 1

43	atg gga agt ctg ccc agc aga aga aaa tct ctg cca agc cca agc ttg	48
44	Met Gly Ser Leu Pro Ser Arg Arg Lys Ser Leu Pro Ser Pro Ser Leu	
45	1 5 10 15	
47	agt tcc tct gtc caa ggc cag gga cct gtg acc atg gaa gca gag aga	96
48	Ser Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg	
49	20 25 30	
51	agc aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt gcc ccg	144
52	Ser Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro	
53	35 40 45	
55	gcc gag ctg tcg ctg aga ctc ggg gag cca ttg acc atc gtc tct gag	192
56	Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu	
57	50 55 60	

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59 gat gga gac tgg tgg acg gtg ctg tct gaa gtc tca ggc aga gag tat      240
60 Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr
61 65              70              75              80
63 aac atc ccc agc gtc cac gtg gcc aaa gtc tcc cat ggg tgg ctg tat      288
64 Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr
65              85              90              95
67 gag ggc ctg agc agg gag aaa gca gag gaa ctg ctg ttg tta cct ggg      336
68 Glu Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Leu Pro Gly
69              100              105              110
71 aac cct gga ggg gcc ttc ctc atc cgg gag agc cag acc agg aga ggc      384
72 Asn Pro Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly
73              115              120              125
75 tct tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg      432
76 Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg
77              130              135              140
79 atc aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc      480
80 Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile
81 145              150              155              160
83 tca ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg gtg gac cat tac      528
84 Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val Asp His Tyr
85              165              170              175
87 tct gag ctg gcg gat gac atc tgc tgc cta ctc aag gag ccc tgt gtc      576
88 Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu Pro Cys Val
89              180              185              190
91 ctg cag agg gct ggc ccg ctc cct ggc aag gat ata ccc cta cct gtg      624
92 Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro Leu Pro Val
93              195              200              205
95 act gtg cag agg aca cca ctc aac tgg aaa gag ctg gac agc tcc ctc      672
96 Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp Ser Ser Leu
97              210              215              220
99 ctg ttt tct gaa gct gcc aca ggg gag gag tct ctt ctc agt gag ggt      720
100 Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu Ser Glu Gly
101 225              230              235              240
103 ctc cgg gag tcc ctc agc ttc tac atc agc ctg aat gac gag gct gtc      768
104 Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp Glu Ala Val
105              245              250              255
107 tct ttg gat gat gcc tag      786
108 Ser Leu Asp Asp Ala
109              260
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 261
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 2
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120 1              5              10              15
123 Ser Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg
124              20              25              30
127 Ser Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro

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128          35          40          45
131 Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu
132          50          55          60
135 Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr
136 65          70          75          80
139 Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr
140          85          90          95
143 Glu Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Leu Pro Gly
144          100          105          110
147 Asn Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly
148          115          120          125
151 Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg
152          130          135          140
155 Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile
156 145          150          155          160
159 Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val Asp His Tyr
160          165          170          175
163 Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu Pro Cys Val
164          180          185          190
167 Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro Leu Pro Val
168          195          200          205
171 Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp Ser Ser Leu
172          210          215          220
175 Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu Ser Glu Gly
176 225          230          235          240
179 Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp Glu Ala Val
180          245          250          255
183 Ser Leu Asp Asp Ala
184          260
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 276
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 3
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198 Pro Asn Pro Glu Gly Leu Asp Ser Asp Phe Leu Ala Val Leu Ser Asp
199          20          25          30
202 Tyr Pro Ser Pro Asp Ile Ser Pro Pro Ile Phe Arg Arg Gly Glu Lys
203          35          40          45
206 Leu Arg Val Ile Ser Asp Glu Gly Gly Trp Trp Lys Ala Ile Ser Leu
207          50          55          60
210 Ser Thr Gly Arg Glu Ser Tyr Ile Pro Gly Ile Cys Val Ala Arg Val
211 65          70          75          80
214 Tyr His Gly Trp Leu Phe Glu Gly Leu Gly Arg Asp Lys Ala Glu Glu
215          85          90          95
218 Leu Leu Gln Leu Pro Asp Thr Lys Val Gly Ser Phe Met Ile Arg Glu
219          100          105          110
222 Ser Glu Thr Lys Lys Gly Phe Tyr Ser Leu Ser Val Arg His Arg Gln

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223          115          120          125
226 Val Lys His Tyr Arg Ile Phe Arg Leu Pro Asn Asn Trp Tyr Tyr Ile
227          130          135          140
230 Ser Pro Arg Leu Thr Phe Gln Cys Leu Glu Asp Leu Val Asn His Tyr
231 145          150          155          160
234 Ser Glu Val Ala Asp Gly Leu Cys Cys Val Leu Thr Thr Pro Cys Leu
235          165          170          175
238 Thr Gln Ser Thr Ala Ala Pro Ala Val Arg Ala Ser Ser Ser Pro Val
239          180          185          190
242 Thr Leu Arg Gln Lys Thr Val Asp Trp Arg Arg Val Ser Arg Leu Gln
243          195          200          205
246 Glu Asp Pro Glu Gly Thr Glu Asn Pro Leu Gly Val Asp Glu Ser Leu
247          210          215          220
250 Phe Ser Tyr Gly Leu Arg Glu Ser Ile Ala Ser Tyr Leu Ser Leu Thr
251 225          230          235          240
254 Ser Glu Asp Asn Thr Ser Phe Asp Arg Lys Lys Lys Ser Ile Ser Leu
255          245          250          255
258 Met Tyr Gly Gly Ser Lys Arg Lys Ser Ser Phe Phe Ser Ser Pro Pro
259          260          265          270
262 Tyr Phe Glu Asp
263          275

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VERIFICATION SUMMARY

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